

SEQ ID NO:1, OLIGO
 G21250/c
 LOCUS G21250 464 bp DNA linear STS 31-MAY-1996
 DEFINITION human STS WI-11603, sequence tagged site.
 ACCESSION G21250
 VERSION G21250.1 GI:1341576
 KEYWORDS STS; STS sequence; primer; sequence tagged site.
 SOURCE Homo sapiens STSs derived from sequences in dbEST and the Unigene collection.

ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 464)
 AUTHORS Hudson,T.
 TITLE Whitehead Institute/MIT Center for Genome Research; Physically Mapped STSs
 JOURNAL Unpublished (1995)
 COMMENT

Contact: Thomas Hudson
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 Whitehead Institute for Biomedical Research
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Primer A: GGGAGTTGATTATGTTGTAGAATCA
 Primer B: AGAAGCGATCAGACCTCTATGC
 STS size: 106
 PCR Profile:

Presoak:
 Denaturation:
 Annealing: 56 degrees C
 Polymerization:
 PCR Cycles: 35
 Thermal Cycler:

Protocol:
 Template: 10 ng
 Primer: each 5 pM
 dNTPs: each 4 nM
 Taq Polymerase: 0.025 units/ul
 Total Vol: 20 ul

Buffer:
 MgCl2: 1.5 mM
 KCl: 50 mM
 Tris-HCL: 10 mM
 pH: 9.3

Derived from dbEST (genbank accession R08904).

FEATURES Location/Qualifiers
 source 1..464
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /map="421.3 cR from top of Chr3 linkage group"
 STS 29..134
 primer_bind 29..53
 primer_bind complement(113..134)

BASE COUNT 101 a 104 c 120 g 130 t 9 others
 ORIGIN

Query Match 16.6%; Score 138; DB 11; Length 464;
 Best Local Similarity 100.0%; Pred. No. 6.1e-54;
 Matches 138; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 694 CTAGCCAAAGCTGGCACAGAAGAAGCAATCGTGTATTTCAGACATAGACCTGAAGAAGCTG 753
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 Db 228 CTAGCCAAAGCTGGCACAGAAGAAGCAATCGTGTATTTCAGACATAGACCTGAAGAAGCTG 169
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 Qy 754 GCTGAAATACGCCAGCAAATCCCCGTTTGTAGACAGAAGCGATCAGACCTCTATGCTGTG 813
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Db 168 GCTGAAATACGCCAGCAAATCCCCGTTTTTAGACAGAAGCGATCAGACCTCTATGCTGTG 109

Qy 814 GAGATGAAAAAGCCCTAA 831

||||||||||||||||

Db 108 GAGATGAAAAAGCCCTAA 91

SEQ ID NO:2, Standard, AA database

Q9NQR4

ID Q9NQR4 PRELIMINARY; PRT; 276 AA.
AC Q9NQR4;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE NIT protein 2 (CUA002).
GN NIT2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX PubMed=10959838;
RA Pace H.C., Hodawadekar S.C., Draganescu A., Huang J., Bieganowski P.,
RA Pekarisky Y., Croce C.M., Brenner C.;
RT "Crystal structure of the worm NitFhit Rosetta Stone protein reveals a
RT Nit tetramer binding two Fhit dimers."
RL Curr. Biol. 10:907-917(2000).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=ADRENOCORTICAL TUMOR SECRETED ACTH;
RA Xu X., Yang Y., Gao G., Xiao H., Chen Z., Han Z.;
RL Submitted (MAY-2000) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AF284574; AAF87103.1; -.
DR EMBL; AF260334; AAG44665.1; -.
DR InterPro; IPR003010; Ntlse/CNhydtse.
DR Pfam; PF00795; CN_hydrolase; 1.
SQ SEQUENCE 276 AA; 30608 MW; 32FA797601A419C6 CRC64;

Query Match 100.0%; Score 1438; DB 4; Length 276;
Best Local Similarity 100.0%; Pred. No. 1.6e-124;
Matches 276; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MTSFRLALIQLQISSIKSDNVTRACSFIREAATQGAKIVSLPECFNSPYGAKYFPEYAEK 60
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Db 1 MTSFRLALIQLQISSIKSDNVTRACSFIREAATQGAKIVSLPECFNSPYGAKYFPEYAEK 60

Qy 61 IPGESTQKLSEVAKECSIYLLIGGSIPEEDAGKLYNTCAVFGPDGTLLAKYRKIHLFDIDV 120
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Db 61 IPGESTQKLSEVAKECSIYLLIGGSIPEEDAGKLYNTCAVFGPDGTLLAKYRKIHLFDIDV 120

Qy 121 PGKITFQESKTLSPGDSFSTFDTPYCRVGLGICYDMRFAELAQIYAQRGCQLLVYPGAFN 180
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Db 121 PGKITFQESKTLSPGDSFSTFDTPYCRVGLGICYDMRFAELAQIYAQRGCQLLVYPGAFN 180

Qy 181 LTTGPAHWELLQRSRAVDNQVYVATASPARDDKASYVAWGHSTVVPWGEVLAKAGTEEA 240
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Db 181 LTTGPAHWELLQRSRAVDNQVYVATASPARDDKASYVAWGHSTVVPWGEVLAKAGTEEA 240

Qy 241 IVYSDIDLKKLAEIRQQIPVFRQKRSPLYAVEMKKP 276
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Db 241 IVYSDIDLKKLAEIRQQIPVFRQKRSPLYAVEMKKP 276

SEQ ID NO:2, Standard

AF284574

LOCUS AF284574 962 bp mRNA linear PRI 24-JUL-2000

DEFINITION Homo sapiens Nit protein 2 (NIT2) mRNA, complete cds.

ACCESSION AF284574

VERSION AF284574.1 GI:9367115

KEYWORDS

SOURCE Homo sapiens.

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 962)

AUTHORS Pace,H.C., Hodawadekar,S.C., Draganescu,A., Huang,J., Bieganski,P., Pekarsky,Y., Croce,C.M. and Brenner,C.

TITLE Crystal structure of the worm NitFhit Rosetta Stone protein reveals a Nit tetramer binding two Fhit dimers

JOURNAL Curr. Biol. 10 (15), 907-917 (2000)

MEDLINE 20414396

PUBMED 10959838

REFERENCE 2 (bases 1 to 962)

AUTHORS Pace,H.C., Hodawadekar,S.C., Draganescu,A., Huang,J., Bieganski,P., Pekarsky,Y., Croce,C.M. and Brenner,C.

TITLE Direct Submission

JOURNAL Submitted (05-JUL-2000) Kimmel Cancer Center, Thomas Jefferson University, 233 S 10th Street, Rm. 826, Philadelphia, PA 19107, USA

FEATURES Location/Qualifiers

source 1..962

/organism="Homo sapiens"

/db_xref="taxon:9606"

gene 1..962

/gene="NIT2"

CDS 22..852

/gene="NIT2"

/note="Nit2; similar to the Nit domains of Caenorhabditis elegans NitFhit and Drosophila melanogaster NitFhit"

/codon_start=1

/product="Nit protein 2"

/protein_id="AAF87103.1"

/db_xref="GI:9367116"

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LAQIYAQRGCQLLVYPGAFNLTTGPAHWELLQRSRAVDNQVYVATASPARDDKASYVA
WGHSTVVPWGEVLAKAGTEEAIVYSDIDLKLAETRQQIPVFRQKRSDLYAVEMKKP
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BASE COUNT 283 a 208 c 218 g 253 t

ORIGIN

Alignment Scores:

Pred. No.: 1.37e-137 Length: 962

Score: 1438.00 Matches: 276

Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0

Query Match: 100.00% Indels: 0

DB: 9 Gaps: 0

US-09-769-952-2 (1-276) x AF284574 (1-962)

QY 1 MetThrSerPheArgLeuAlaLeuIleGlnLeuGlnIleSerSerIleLysSerAspAsn 20

Db 22 ATGACCTCTTTCGCTTGGCCCTCATCCAGCTTCAGATTCTTCCATCAAATCAGATAAC 81

QY 21 ValThrArgAlaCysSerPheIleArgGluAlaAlaThrGlnGlyAlaLysIleValSer 40

Db 82 GTCACCTCGCGCTTGTAGCTTCATCCGGGAGGAGCAACGCAAGGAGCCAAATAGTTTCT 141

QY 41 LeuProGluCysPheAsnSerProTyrGlyAlaLysTyrPheProGluTyrAlaGluLys 60

Db 142 TTGCCGGAATGCTTTAATTCTCCATATGGAGCGAAATATTTCTGAATATGCAGAGAAA 201

QY 61 IleProGlyGluSerThrGlnLysLeuSerGluValAlaLysGluCysSerIleTyrLeu 80

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Db 202 ATTCCTGGTGAATCCACACAGAAGCTTTCTGAAGTAGCAAAGGAATGCAGCATATATCTC 261
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Qy 81 IleGlyGlySerIleProGluGluAspAlaGlyLysLeuTyrAsnThrCysAlaValPhe 100
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Db 262 ATTGGAGGCTCTATCCCTGAAGAGGATGCTGGGAAATTATATAACACCTGTGCTGTGTTT 321
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Qy 101 GlyProAspGlyThrLeuLeuAlaLysTyrArgLysIleHisLeuPheAspIleAspVal 120
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Qy 121 ProGlyLysIleThrPheGlnGluSerLysThrLeuSerProGlyAspSerPheSerThr 140
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Db 382 CCTGGAAAAATTACATTTCAAGAATCTAAACATTGAGTCCGGGTGATAGTTTCTCCACA 441
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Qy 141 PheAspThrProTyrCysArgValGlyLeuGlyIleCysTyrAspMetArgPheAlaGlu 160
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Db 442 TTTGATACTCCTTACTGCAGAGTGGGTCTGGGCATCTGCTACGACATGCGGTTGCAGAG 501
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Qy 161 LeuAlaGlnIleTyrAlaGlnArgGlyCysGlnLeuLeuValTyrProGlyAlaPheAsn 180
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Db 502 CTTGCACAAATCTACGCACAGAGAGGCTGCCAGCTGTTGGTATATCCAGGAGCTTTTAAT 561
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Db 562 CTGACCACTGGACCAGCCATTGGGAGTTACTTCAGCGAAGCCGGGCTGTTGATAATCAG 621
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Qy 201 ValTyrValAlaThrAlaSerProAlaArgAspAspLysAlaSerTyrValAlaTrpGly 220
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Db 622 GTGTATGTGGCCACAGCCTCTCCTGCCCGGGATGACAAAGCCTCCTATGTTGCCTGGGGA 681
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Qy 221 HisSerThrValValAsnProTrpGlyGluValLeuAlaLysAlaGlyThrGluGluAla 240
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Db 682 CACAGCACCGTGGTGAACCCTTGGGGGGAGGTTCTAGCCAAAGCTGGCACAGAAGAAGCA 741
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Qy 241 IleValTyrSerAspIleAspLeuLysLysLeuAlaGluIleArgGlnGlnIleProVal 260
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Db 742 ATCGTGATTTCAGACATAGACCTGAAGAAGCTGGCTGAAATACGCCAGCAATCCCCGTT 801
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Qy 261 PheArgGlnLysArgSerAspLeuTyrAlaValGluMetLysLysPro 276
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Db 802 TTTAGACAGAAGCGATCAGACCTCTATGCTGTGGAGATGAAAAGCCC 849

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